

Sequence Listing

<110> Baker, Kevin
 Botstein, David
 Eaton, Dan
 Ferrara, Napoleone
 Filvaroff, Ellen
 Gerritsen, Mary
 Goddard, Audrey
 Godowski, Paul
 Grimaldi, Christopher
 Gurney, Austin
 Hillan, Kenneth
 Kljavin, Ivar
 Napier, Mary
 Roy, Margaret
 Tumas, Daniel
 Wood, William

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<213> Homo Sapien

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35 40 45
Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
50 55 60
Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
65 70 75
Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
80 85 90
Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
95 100 105
Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
110 115 120
Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
125 130 135
Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
140 145 150
Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
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170 175 180
Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
185 190 195
Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
200 205 210

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Ile Ala Glu Ala Lys Leu Thr Ser Val Pro Lys Gly Leu Pro Pro	230	235	240
Thr Leu Leu Glu Leu His Leu Asp Tyr Asn Lys Ile Ser Thr Val	245	250	255
Glu Leu Glu Asp Phe Lys Arg Tyr Lys Glu Leu Gln Arg Leu Gly	260	265	270
Leu Gly Asn Asn Lys Ile Thr Asp Ile Glu Asn Gly Ser Leu Ala	275	280	285
Asn Ile Pro Arg Val Arg Glu Ile His Leu Glu Asn Asn Lys Leu	290	295	300
Lys Lys Ile Pro Ser Gly Leu Pro Glu Leu Lys Tyr Leu Gln Ile	305	310	315
Ile Phe Leu His Ser Asn Ser Ile Ala Arg Val Gly Val Asn Asp	320	325	330
Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu Tyr Ser Ala	335	340	345
Ile Ser Leu Phe Asn Asn Pro Val Lys Tyr Trp Glu Met Gln Pro	350	355	360
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<220>
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<212> PRT
<213> Homo Sapien

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35 40 45
Arg Gly Ala Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu
50 55 60
Asp Glu Thr Trp His Pro Asp Leu Gly Gln Pro Phe Gly Val Met
65 70 75

Arg Cys Val Leu Cys Ala Cys Glu Ala Pro Gln Trp Gly Arg Arg	80	85	90
Thr Arg Gly Pro Gly Arg Val Ser Cys Lys Asn Ile Lys Pro Glu	95	100	105
Cys Pro Thr Pro Ala Cys Gly Gln Pro Arg Gln Leu Pro Gly His	110	115	120
Cys Cys Gln Thr Cys Pro Gln Glu Arg Ser Ser Ser Glu Arg Gln	125	130	135
Pro Ser Gly Leu Ser Phe Glu Tyr Pro Arg Asp Pro Glu His Arg	140	145	150
Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala Glu Glu Arg Ala Arg	155	160	165
Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu Thr Gly Pro Arg	170	175	180
Ser Gln Ala Val Ala Arg Ala Arg Val Ser Leu Leu Arg Ser Ser	185	190	195
Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro Thr Arg	200	205	210
Ile Arg Phe Ser Asp Ser Asn Gly Ser Val Leu Phe Glu His Pro	215	220	225
Ala Ala Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala	230	235	240
Val Pro Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu His	245	250	255
Val Ala Leu Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly	260	265	270
Pro Leu Ile Arg His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala	275	280	285
Ile Leu Thr Leu Glu Gly Pro Pro Gln Gln Gly Val Gly Gly Ile	290	295	300
Thr Leu Leu Thr Leu Ser Asp Thr Glu Asp Ser Leu His Phe Leu	305	310	315
Leu Leu Phe Arg Gly Leu Leu Glu Pro Arg Ser Gly Gly Leu Thr	320	325	330
Gln Val Pro Leu Arg Leu Gln Ile Leu His Gln Gly Gln Leu Leu	335	340	345
Arg Glu Leu Gln Ala Asn Val Ser Ala Gln Glu Pro Gly Phe Ala	350	355	360
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Ser	Leu	Ile	Tyr	Gln	Val	Gln	Val	Val	Gly	Thr	Ser	Ser	Glu	Val					
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Pro	Asp	Gly	Glu	Leu	Arg	Gly	His	Val	Ala	Ala	Leu	Pro	Tyr	Cys					
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Gly	His	Ser	Ala	Arg	His	Asp	Thr	Leu	Pro	Val	Pro	Leu	Ala	Gly					
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Ala	Leu	Val	Leu	Pro	Pro	Val	Lys	Ser	Gln	Ala	Ala	Gly	His	Ala					
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<400> 12
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<400> 13
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<210> 14
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<212> DNA
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<212> PRT

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35 40 45

Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr
50 55 60

Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Glu
65 70 75

Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn
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Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His
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Gly Asn Cys Ser Ser Ser Ser Ser Ser Ser Ser Asp Gly Tyr Leu

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<212> PRT

<213> Homo Sapien

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<210> 29

<211> 1416

<212> DNA

<213> Homo Sapien

<400> 29

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gcctgatgc gggacttccc gctcgtggac ggccacaacg acctgcccct 200

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ggcgcccagt tctggtcage ctatgtgcca tgccagaccc aggaccggga 350

tgccctgcgc ctcaccctgg agcagattga cctcatacgc cgcgatgtgtg 400

cctcctattc tgagctggag cttgtgacct cggctaaaagc tctgaacgac 450
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<210> 30
 <211> 446
 <212> PRT
 <213> Homo Sapien

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 35 40 45
 Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

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Tyr	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	Gly
				65					70					75
Ala	Gln	Phe	Trp	Ser	Ala	Tyr	Val	Pro	Cys	Gln	Thr	Gln	Asp	Arg
				80					85					90
Asp	Ala	Leu	Arg	Leu	Thr	Leu	Glu	Gln	Ile	Asp	Leu	Ile	Arg	Arg
				95					100					105
Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	Lys
				110					115					120
Ala	Leu	Asn	Asp	Thr	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	Glu
				125					130					135
Gly	Gly	His	Ser	Leu	Asp	Asn	Ser	Leu	Ser	Ile	Leu	Arg	Thr	Phe
				140					145					150
Tyr	Met	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	His	Thr	Cys	Asn
				155					160					165
Thr	Pro	Trp	Ala	Glu	Ser	Ser	Ala	Lys	Gly	Val	His	Ser	Phe	Tyr
				170					175					180
Asn	Asn	Ile	Ser	Gly	Leu	Thr	Asp	Phe	Gly	Glu	Lys	Val	Val	Ala
				185					190					195
Glu	Met	Asn	Arg	Leu	Gly	Met	Met	Val	Asp	Leu	Ser	His	Val	Ser
				200					205					210
Asp	Ala	Val	Ala	Arg	Arg	Ala	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val
				215					220					225
Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Gly	Val	Cys	Asn	Ser	Ala	Arg
				230					235					240
Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly
				245					250					255
Val	Val	Met	Val	Ser	Leu	Ser	Met	Gly	Val	Ile	Gln	Cys	Asn	Pro
				260					265					270
Ser	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Lys
				275					280					285
Ala	Val	Ile	Gly	Ser	Lys	Phe	Ile	Gly	Ile	Gly	Gly	Asp	Tyr	Asp
				290					295					300
Gly	Ala	Gly	Lys	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr
				305					310					315
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Gly	Trp	Ser	Glu	Glu
				320					325					330
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg
				335					340					345

Gln Val Glu Lys	Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu	
350	355	360
Glu Asp Lys Phe	Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser	
365	370	375
Asp Leu Ser Arg	Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln	
380	385	390
Glu Leu Thr Glu	Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala	
395	400	405
Lys Trp Ser Val	Ser Glu Ser Ser Pro His Pro Asp Lys Thr His	
410	415	420
Thr Cys Pro Pro	Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser	
425	430	435
Val Phe Leu Phe	Pro Pro Lys Pro Lys Asp Thr	
440	445	

<210> 31
 <211> 1790
 <212> DNA
 <213> Homo Sapien

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 atccgcgcgg cgccgcgcgc cgttgctgcc cctgctgctg ctgctctgcg 200
 tcctcggggc gccgcgagcc ggatcaggag ccacacagc tgtgatcagt 250
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 agtgcacgga gaccaccag gagccaccgc cgagggcctc tactggaccc 350
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 atggccagga caacacatgt gaggagtacc acacagtggg gcccactcc 700
 tgccacatcc ccaaggacct ggctctcttt acgccctatg agatctgggt 750
 ggaggccacc aaccgcctgg gctctgcccc ctccgatgta ctcacgctgg 800

Country	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (%)	Urban population growth rate (%)
Algeria	1980	12.5	4.5	36	100	100	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	1985	13.5	5.5	41	110	110	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	1990	14.5	6.5	45	120	120	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	1995	15.5	7.5	48	130	130	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2000	16.5	8.5	51	140	140	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2005	17.5	9.5	54	150	150	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2010	18.5	10.5	57	160	160	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2015	19.5	11.5	59	170	170	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2020	20.5	12.5	61	180	180	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2025	21.5	13.5	63	190	190	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2030	22.5	14.5	64	200	200	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2035	23.5	15.5	66	210	210	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2040	24.5	16.5	67	220	220	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2045	25.5	17.5	69	230	230	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2050	26.5	18.5	70	240	240	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2055	27.5	19.5	71	250	250	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2060	28.5	20.5	72	260	260	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2065	29.5	21.5	73	270	270	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2070	30.5	22.5	74	280	280	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2075	31.5	23.5	75	290	290	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2080	32.5	24.5	76	300	300	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2085	33.5	25.5	76	310	310	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2090	34.5	26.5	77	320	320	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2095	35.5	27.5	78	330	330	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2100	36.5	28.5	78	340	340	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2105	37.5	29.5	79	350	350	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2110	38.5	30.5	79	360	360	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2115	39.5	31.5	80	370	370	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2120	40.5	32.5	80	380	380	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2125	41.5	33.5	81	390	390	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2130	42.5	34.5	81	400	400	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2135	43.5	35.5									

<211> 422

<213> Homo Sapien

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Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys
50 55 60

Ser	Val	His	Gly	Asp	Pro	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr	65	70	75
Trp	Thr	Leu	Asn	Gly	Arg	Arg	Leu	Pro	Pro	Glu	Leu	Ser	Arg	Val	80	85	90
Leu	Asn	Ala	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	95	100	105
Ser	Arg	Gln	Arg	Ser	Gly	Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	110	115	120
Gly	Ser	Ile	Leu	Ala	Gly	Ser	Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	125	130	135
Glu	Lys	Pro	Val	Asn	Ile	Ser	Cys	Trp	Ser	Lys	Asn	Met	Lys	Asp	140	145	150
Leu	Thr	Cys	Arg	Trp	Thr	Pro	Gly	Ala	His	Gly	Glu	Thr	Phe	Leu	155	160	165
His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln	170	175	180
Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr	Val	Gly	Pro	His	Ser	Cys	185	190	195
His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr	Glu	Ile	Trp	200	205	210
Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp	Val	Leu	215	220	225
Thr	Leu	Asp	Ile	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro	Asp	230	235	240
Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu	Ser	Val	245	250	255
Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala	260	265	270
Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys	275	280	285
Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	290	295	300
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	305	310	315
Phe	Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	320	325	330
Ser	His	Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	335	340	345
Pro	Gly	Gly	Gly	Ala	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser			

350	355	360
Gly Pro Val Arg	Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys	
365	370	375
Lys His Ala Tyr	Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln	
380	385	390
Trp Arg Ala Trp	Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp	
395	400	405
Glu Gly Ile Leu	Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro	
410	415	420
Ala Arg		

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<220>
 <223> Synthetic oligonucleotide probe

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<210> 34
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<220>
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<210> 35
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<210> 36
 <211> 1771
 <212> DNA
 <213> Homo Sapien

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ctccctagag	tccttcgtga	agctttttat	tcctaagagg	agaaaatcag	200
tcaccggcga	aatcgtgctg	attacaggag	ctgggcatgg	aattgggaga	250
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tataaataag	catggactgg	aggaaacagc	tgccaaatgc	aagggactgg	350
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1. **Background:** The purpose of this study was to evaluate the effect of a 12-week supervised exercise program on the physical and psychological health of individuals with chronic low back pain (CLBP). The study was conducted in a community-based setting.

2. **Methods:** A total of 100 individuals with CLBP were recruited from a community-based setting. They were randomly assigned to either a supervised exercise program (n=50) or a control group (n=50). The supervised exercise program consisted of 12 weeks of supervised exercise, including aerobic and strength training. The control group received no intervention.

3. **Results:** The supervised exercise program significantly improved physical and psychological health outcomes compared to the control group. The supervised exercise group showed significant improvements in pain intensity, functional status, and quality of life. The control group showed no significant changes in these outcomes.

4. **Conclusion:** A 12-week supervised exercise program significantly improved physical and psychological health outcomes in individuals with CLBP. This study suggests that supervised exercise is an effective intervention for CLBP.

5. **Keywords:** Chronic low back pain, supervised exercise, physical health, psychological health, community-based setting.

<400> 37

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215	220	225
Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu		
230	235	240
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys		
245	250	255
Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu		
260	265	270
Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile		
275	280	285
Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln		
290	295	300

<210> 38

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<212> DNA

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<400> 42

Met	Arg	Pro	Leu	Leu	Val	Leu	Leu	Leu	Leu	Gly	Leu	Ala	Ala	Gly	1	5	10	15
Ser	Pro	Pro	Leu	Asp	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro	Gly	20	25	30	
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly	35	40	45	
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly	50	55	60	
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly	65	70	75	
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly	80	85	90	
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala	95	100	105	
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp	110	115	120	
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His	125	130	135	
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val	140	145	150	
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln	155	160	165	
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln	170	175	180	
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala	185	190	195	
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly	200	205	210	
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser	215	220	225	
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro	230	235	240	
Val	Phe	Ala																

<210> 43
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 43
 tacaggccca gtcaggacca gggg 24

 <210> 44
 <211> 18
 <212> DNA
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 <223> Synthetic oligonucleotide probe

 <400> 44
 agccagcctc gctctcgg 18

 <210> 45
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 45
 gtctgcgatc aggtctgg 18

 <210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 46
 gaaagaggca atggattcgc 20

 <210> 47
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 47
 gattacact tgccagcaca gcac 24

 <210> 48
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49

<211> 1876

<212> DNA

<213> Homo Sapien

<400> 49

ctcttttgtc caccagccca gcctgactcc tggagattgt gaatagctcc 50
atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100
acctgacggg cccaacagac ccattgctga tccagagacc tcccctggcc 150
gggggcatct cctggctgtg ctccctggccc tccttggcac cacctgggca 200
gagggtgtggc caccacagct gcaggagcag gctccgatgg ccggagccct 250
gaacaggaag gagagtttct tgctcctctc cctgcacaac cgcttgcgca 300
gctgggtcca gcccctgctg gctgacatgc ggaggctgga ctggagtgc 350
agcctggccc aactggctca agccaggga gccctctgtg gaatcccaac 400
cccgagcctg gcattcggcc tgtggcgcac cctgcaagtg ggctggaaca 450
tgcagctgct gcccgcgggc ttggcgctct ttgttgaagt ggtcagccta 500
tggtttgcag aggggcagcg gtacagccac gcggcaggag agtgtgctcg 550
caacgccacc tgcaccact acacgcagct cgtgtgggccc acctcaagcc 600
agctgggctg tgggcggcac ctgtgctctg caggccagac agcgatagaa 650
gcctttgtct gtgcctactc ccccgagggc aactgggagg tcaacgggaa 700
gacaatcatt ccctataaga aggggtgctg gtgttcgctc tgcacagcca 750
gtgtctcagg ctgcttcaaa gcctgggacc atgcaggggg gctctgtgag 800
gtccccagga atccttgtcg catgagctgc cagaacctg gacgtctcaa 850
catcagcacc tgccactgcc actgtcccc tggctacacg ggagatact 900
gccaagtgcg gtgcagcctg cagtgtgtgc acggccggtt ccgggaggag 950
gagtgtctcg gcgtctgtga catcggctac gggggagccc agtgtgccac 1000
caaggtgcat ttcccttcc acacctgtga cctgaggatc gacggagact 1050
gcttcatggt gtcttcagag gcagacacct attacagagc caggatgaaa 1100
tgtcagagga aaggcggggt gctggcccag atcaagagcc agaaagtgc 1150

[illegible]

<211> 455

<213> Homo Sapien

Met Leu His Pro Glu Thr Ser Pro Gly Arg Gly His Leu Leu Ala
1 5 10 15

Pro Gln Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg
35 40 45

Trp Val Gln Pro Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser
65 70 75

Ile Pro Thr Pro Ser Leu Ala Ser Gly Leu Trp Arg Thr Leu Gln
95 100 105

38

				110					115					120
Val	Glu	Val	Val	Ser 125	Leu	Trp	Phe	Ala	Glu 130	Gly	Gln	Arg	Tyr	Ser 135
His	Ala	Ala	Gly	Glu 140	Cys	Ala	Arg	Asn	Ala 145	Thr	Cys	Thr	His	Tyr 150
Thr	Gln	Leu	Val	Trp 155	Ala	Thr	Ser	Ser	Gln 160	Leu	Gly	Cys	Gly	Arg 165
His	Leu	Cys	Ser	Ala 170	Gly	Gln	Thr	Ala	Ile 175	Glu	Ala	Phe	Val	Cys 180
Ala	Tyr	Ser	Pro	Gly 185	Gly	Asn	Trp	Glu	Val 190	Asn	Gly	Lys	Thr	Ile 195
Ile	Pro	Tyr	Lys	Lys 200	Gly	Ala	Trp	Cys	Ser 205	Leu	Cys	Thr	Ala	Ser 210
Val	Ser	Gly	Cys	Phe 215	Lys	Ala	Trp	Asp	His 220	Ala	Gly	Gly	Leu	Cys 225
Glu	Val	Pro	Arg	Asn 230	Pro	Cys	Arg	Met	Ser 235	Cys	Gln	Asn	His	Gly 240
Arg	Leu	Asn	Ile	Ser 245	Thr	Cys	His	Cys	His 250	Cys	Pro	Pro	Gly	Tyr 255
Thr	Gly	Arg	Tyr	Cys 260	Gln	Val	Arg	Cys	Ser 265	Leu	Gln	Cys	Val	His 270
Gly	Arg	Phe	Arg	Glu 275	Glu	Glu	Cys	Ser	Cys 280	Val	Cys	Asp	Ile	Gly 285
Tyr	Gly	Gly	Ala	Gln 290	Cys	Ala	Thr	Lys	Val 295	His	Phe	Pro	Phe	His 300
Thr	Cys	Asp	Leu	Arg 305	Ile	Asp	Gly	Asp	Cys 310	Phe	Met	Val	Ser	Ser 315
Glu	Ala	Asp	Thr	Tyr 320	Tyr	Arg	Ala	Arg	Met 325	Lys	Cys	Gln	Arg	Lys 330
Gly	Gly	Val	Leu	Ala 335	Gln	Ile	Lys	Ser	Gln 340	Lys	Val	Gln	Asp	Ile 345
Leu	Ala	Phe	Tyr	Leu 350	Gly	Arg	Leu	Glu	Thr 355	Thr	Asn	Glu	Val	Thr 360
Asp	Ser	Asp	Phe	Glu 365	Thr	Arg	Asn	Phe	Trp 370	Ile	Gly	Leu	Thr	Tyr 375
Lys	Thr	Ala	Lys	Asp 380	Ser	Phe	Arg	Trp	Ala 385	Thr	Gly	Glu	His	Gln 390
Ala	Phe	Thr	Ser	Phe 395	Ala	Phe	Gly	Gln	Pro 400	Asp	Asn	His	Gly	Leu 405

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg
440 445 450

Trp Gly Pro Gly Ser
455

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 51
aggaacttct ggatcgggct cacc 24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 52
gggtctgggc caggtggaag agag 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
gccaaggact cttccgctg ggccacagg gagcaccagg cttc 45

<210> 54
<211> 2331
<212> DNA
<213> Homo Sapien

<400> 54
cggacgcgtg ggctgggcgc tgcaaagcgt gtcccgccgg gtcccgagc 50
gtcccgccgc ctgccccgc catgctctg ctgctggggc tgtgcctggg 100
gctgtccctg tgtgtggggc cgcaggaaga ggcgagagc tggggccact 150
cttcggagca ggatggactc agggccccga ggcaagtcag actgttgacg 200

aggctgaaaa ccaaaccctt gatgacagaa ttctcagtga agtctacat 250
catttcccgt tatgccttca ctacggtttc ctgcagaatg ctgaacagag 300
cttctgaaga ccaggacatt gagttccaga tgcagattcc agctgcagct 350
ttcatcacca acttcactat gcttattgga gacaagggtg atcagggcga 400
aattacagag agagaaaaga agagtgggtga tagggtaaaa gagaaaagga 450
ataaaaccac agaagaaaat ggagagaagg ggactgaaat attcagagct 500
tctgcagtga ttcccagcaa ggacaaagcc gcctttttcc tgagttatga 550
ggagcttctg cagaggcgcc tgggcaagta cgagcacagc atcagcgtgc 600
ggccccagca gctgtccggg aggctgagcg tggacgtgaa tatectggag 650
agcgcgggca tgcacccct ggaggtgctg ccgcttcaca acagcaggca 700
gaggggcagt gggcgcgggg aagatgattc tgggcctccc ccatctactg 750
tcattaacca aaatgaaaca ttgccaaca taatttttaa acctactgta 800
gtacaacaag ccaggattgc ccagaatgga attttgggag actttatcat 850
tagatatgac gtcaatagag aacagagcat tggggacatc caggttctaa 900
atggctatct tgtgcactac ttgtctcta aagaccttc tcttttacc 950
aagaatgtgg tattegtgct tgacagcagt gcttctatgg tgggaaccaa 1000
actccggcag accaaggatg cctcttcac aattctccat gacctccgac 1050
cccaggaccg ttctagtatc attggatttt ccaaccgatg caaagtatgg 1100
aaggaccact tgatatcagt cactccagac agcatcaggg atgggaaagt 1150
gtacattcac catatgtcac ccactggagg cacagacatc aacggggccc 1200
tgcagagggc catcaggctc ctcaacaagt acgtggccca cagtggcatt 1250
ggagaccgga gcgtgtccct catcgtcttc ctgacggatg ggaagcccac 1300
ggtcggggag acgcacaccc tcaagatcct caacaacacc cgagaggccg 1350
cccagggcca agtctgcac ttaccattg gcatcgcaa cgacgtggac 1400
ttcaggctgc tggagaaact gtcgtggag aactgtggcc tcacacggcg 1450
cgtgcacgag gaggaggacg caggctcgca gctcatcggg ttctacgatg 1500
aaatcaggac cccgtcttc tctgacatcc gcatcgatta tccccccagc 1550
tcagtgggtg aggccaccaa gacctgttc cccaactact tcaacggctc 1600
ggagatcatc attgcgggga agctgggtgga caggaagctg gatcacctgc 1650

Variable	Mean	SD	Min	Max
Age	38.5	10.5	25	55
Gender	Male	Female		
Marital status	Married	Single		
Education	High school	College		
Occupation	Manager	Worker		
Income	Low	High		
Health status	Good	Poor		
Stress level	Low	High		
Life satisfaction	High	Low		
Resilience	High	Low		
Optimism	High	Low		
Self-efficacy	High	Low		
Perceived stress	Low	High		
Depression	Low	High		
Anxiety	Low	High		
Quality of life	High	Low		
Health-related quality of life	High	Low		
Physical health	High	Low		
Mental health	High	Low		
Social health	High	Low		
Overall health	High	Low		

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<400> 55
Met Leu Leu Leu Leu Gly Leu Cys Leu Gly Leu Ser Leu Cys Val
  1                      5                      10                      15

Gly Ser Gln Glu Glu Ala Gln Ser Trp Gly His Ser Ser Glu Gln
                      20                      25                      30

Asp Gly Leu Arg Val Pro Arg Gln Val Arg Leu Leu Gln Arg Leu
                      35                      40                      45

Lys Thr Lys Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile
                      50                      55                      60

Ile Ser Arg Tyr Ala Phe Thr Thr Val Ser Cys Arg Met Leu Asn
                      65                      70                      75

Arg Ala Ser Glu Asp Gln Asp Ile Glu Phe Gln Met Gln Ile Pro
                      80                      85                      90

Ala Ala Ala Phe Ile Thr Asn Phe Thr Met Leu Ile Gly Asp Lys
                      95                      100                     105

Val Tyr Gln Gly Glu Ile Thr Glu Arg Glu Lys Lys Ser Gly Asp
                      110                      115                      120

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Arg Val Lys Glu	Lys Arg Asn Lys Thr	Thr Glu Glu Asn Gly Glu	125	130	135
Lys Gly Thr Glu	Ile Phe Arg Ala Ser	Ala Val Ile Pro Ser Lys	140	145	150
Asp Lys Ala Ala	Phe Phe Leu Ser Tyr	Glu Glu Leu Leu Gln Arg	155	160	165
Arg Leu Gly Lys	Tyr Glu His Ser Ile	Ser Val Arg Pro Gln Gln	170	175	180
Leu Ser Gly Arg	Leu Ser Val Asp Val	Asn Ile Leu Glu Ser Ala	185	190	195
Gly Ile Ala Ser	Leu Glu Val Leu Pro	Leu His Asn Ser Arg Gln	200	205	210
Arg Gly Ser Gly	Arg Gly Glu Asp Asp	Ser Gly Pro Pro Pro Ser	215	220	225
Thr Val Ile Asn	Gln Asn Glu Thr Phe	Ala Asn Ile Ile Phe Lys	230	235	240
Pro Thr Val Val	Gln Gln Ala Arg Ile	Ala Gln Asn Gly Ile Leu	245	250	255
Gly Asp Phe Ile	Ile Arg Tyr Asp Val	Asn Arg Glu Gln Ser Ile	260	265	270
Gly Asp Ile Gln	Val Leu Asn Gly Tyr	Phe Val His Tyr Phe Ala	275	280	285
Pro Lys Asp Leu	Pro Pro Leu Pro Lys	Asn Val Val Phe Val Leu	290	295	300
Asp Ser Ser Ala	Ser Met Val Gly Thr	Lys Leu Arg Gln Thr Lys	305	310	315
Asp Ala Leu Phe	Thr Ile Leu His Asp	Leu Arg Pro Gln Asp Arg	320	325	330
Phe Ser Ile Ile	Gly Phe Ser Asn Arg	Ile Lys Val Trp Lys Asp	335	340	345
His Leu Ile Ser	Val Thr Pro Asp Ser	Ile Arg Asp Gly Lys Val	350	355	360
Tyr Ile His His	Met Ser Pro Thr Gly	Gly Thr Asp Ile Asn Gly	365	370	375
Ala Leu Gln Arg	Ala Ile Arg Leu Leu	Asn Lys Tyr Val Ala His	380	385	390
Ser Gly Ile Gly	Asp Arg Ser Val Ser	Leu Ile Val Phe Leu Thr	395	400	405
Asp Gly Lys Pro	Thr Val Gly Glu Thr	His Thr Leu Lys Ile Leu			

410	415	420
Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr		
425	430	435
Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu		
440	445	450
Ser Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Glu Glu Glu		
455	460	465
Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr		
470	475	480
Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val		
485	490	495
Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser		
500	505	510
Glu Ile Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His		
515	520	525
Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile		
530	535	540
Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp		
545	550	555
Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Thr		
560	565	570
Asn His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu		
575	580	585
Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg		
590	595	600
Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu		
605	610	615
Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met		
620	625	630
Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met Gly Pro		
635	640	645
Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro Gly		
650	655	660
Pro Leu Leu Lys Lys Pro Asn Ser Val Lys Lys Lys Gln Asn Lys		
665	670	675
Thr Lys Lys Arg His Gly Arg Asp Gly Val Phe Pro Leu His His		
680	685	690
Leu Gly Ile Arg		

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
gtgggaacca aactccggca gacc 24

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
cacatcgagc gtctctgg 18

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 58
agccgctcct tctccggttc atcg 24

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
tggaaggacc acttgatata agtcactcca gacagcatca gggatggg 48

<210> 60
<211> 1413
<212> DNA
<213> Homo Sapien

<400> 60
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ccagtgtgcg gcggcagcgg cggcggcggc gcctcccggg ctccggcttc 100
tgctgttgct cttctccgcc gcggcactga tccccacagg tgatgggcag 150
aatctgttta cgaaagacgt gacagtgatc gagggagagg ttgcgacat 200

cagttgccaa gtcaataaga gtgacgactc tgtgattcag ctactgaatc 250
ccaacaggca gaccatttat ttcagggact tcaggccttt gaaggacagc 300
aggtttcagt tgctgaatth ttctagcagt gaactcaaag tatcattgac 350
aaacgtctca atttctgatg aaggaagata cttttgccag ctctataaccg 400
atccccca gaaaggttac accaccatca cagtcctggt cccaccacgt 450
aatctgatga tcgatatcca gaaagacact gcggtggaag gtgaggagat 500
tgaagtcaac tgcactgcta tggccagcaa gccagccacg actatcaggt 550
ggttcaaagg gaacacagag ctaaaaggca aatcggaggt ggaagagtgg 600
tcagacatgt aactgtgac cagtcagctg atgctgaagg tgcacaagga 650
ggacgatggg gtcccagtga tctgccaggt ggagcaccct gcggtcactg 700
gaaacctgca gaccagcgg tatctagaag tacagtataa gcctcaagtg 750
cacattcaga tgacttatcc tctacaaggc ttaaccggg aaggggacgc 800
gcttgagtta acatgtgaag ccatcgggaa gcccagcct gtgatggtaa 850
cttgggtgag agtcgatgat gaaatgcctc aacacgccgt actgtctggg 900
cccaacctgt tcatcaataa cctaaacaaa acagataatg gtacataaccg 950
ctgtgaagct tcaaacatag tggggaaagc tcaactcgat tatatgctgt 1000
atgtatacga tccccca actatccctc ctcccacaac aaccaccacc 1050
accaccacca ccaccaccac caccatcctt accatcatca cagattccccg 1100
agcaggtgaa gaaggctcga tcagggcagt ggatcatgcc gtgatcgggtg 1150
gcgtcgtggc ggtggtggtg ttcgccatgc tgtgcttget catcattctg 1200
gggcgctatt ttgccagaca taaaggtaaa tacttcactc atgaagccaa 1250
aggagccgat gacgcagcag acgcagacac agctataatc aatgcagaag 1300
gaggacagaa caactccgaa gaaaagaaag agtacttcat ctagatcagc 1350
ctttttgttt caatgaggtg tccaactggc cctatttaga tgataaagag 1400
acagtgatat tgg 1413

<210> 61

<211> 440

<212> PRT

<213> Homo Sapien

<400> 61

Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala
1 5 10 15

Ala	Ala	Ala	Ala	Ala 20	Pro	Pro	Gly	Leu	Arg 25	Leu	Leu	Leu	Leu	Leu 30
Phe	Ser	Ala	Ala	Ala 35	Leu	Ile	Pro	Thr	Gly 40	Asp	Gly	Gln	Asn	Leu 45
Phe	Thr	Lys	Asp	Val 50	Thr	Val	Ile	Glu	Gly 55	Glu	Val	Ala	Thr	Ile 60
Ser	Cys	Gln	Val	Asn 65	Lys	Ser	Asp	Asp	Ser 70	Val	Ile	Gln	Leu	Leu 75
Asn	Pro	Asn	Arg	Gln 80	Thr	Ile	Tyr	Phe	Arg 85	Asp	Phe	Arg	Pro	Leu 90
Lys	Asp	Ser	Arg	Phe 95	Gln	Leu	Leu	Asn	Phe 100	Ser	Ser	Ser	Glu	Leu 105
Lys	Val	Ser	Leu	Thr 110	Asn	Val	Ser	Ile	Ser 115	Asp	Glu	Gly	Arg	Tyr 120
Phe	Cys	Gln	Leu	Tyr 125	Thr	Asp	Pro	Pro	Gln 130	Glu	Ser	Tyr	Thr	Thr 135
Ile	Thr	Val	Leu	Val 140	Pro	Pro	Arg	Asn	Leu 145	Met	Ile	Asp	Ile	Gln 150
Lys	Asp	Thr	Ala	Val 155	Glu	Gly	Glu	Glu	Ile 160	Glu	Val	Asn	Cys	Thr 165
Ala	Met	Ala	Ser	Lys 170	Pro	Ala	Thr	Thr	Ile 175	Arg	Trp	Phe	Lys	Gly 180
Asn	Thr	Glu	Leu	Lys 185	Gly	Lys	Ser	Glu	Val 190	Glu	Glu	Trp	Ser	Asp 195
Met	Tyr	Thr	Val	Thr 200	Ser	Gln	Leu	Met	Leu 205	Lys	Val	His	Lys	Glu 210
Asp	Asp	Gly	Val	Pro 215	Val	Ile	Cys	Gln	Val 220	Glu	His	Pro	Ala	Val 225
Thr	Gly	Asn	Leu	Gln 230	Thr	Gln	Arg	Tyr	Leu 235	Glu	Val	Gln	Tyr	Lys 240
Pro	Gln	Val	His	Ile 245	Gln	Met	Thr	Tyr	Pro 250	Leu	Gln	Gly	Leu	Thr 255
Arg	Glu	Gly	Asp	Ala 260	Leu	Glu	Leu	Thr	Cys 265	Glu	Ala	Ile	Gly	Lys 270
Pro	Gln	Pro	Val	Met 275	Val	Thr	Trp	Val	Arg 280	Val	Asp	Asp	Glu	Met 285
Pro	Gln	His	Ala	Val 290	Leu	Ser	Gly	Pro	Asn 295	Leu	Phe	Ile	Asn	Asn 300
Leu	Asn	Lys	Thr	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ser	Asn

[illegible]

<220>
<223> Synthetic oligonucleotide probe

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<210> 63
<211> 20
<212> DNA
<213> Artificial Sequence
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<400> 63
gtacactgtg accagtcagc 20
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<220>
<223> Synthetic oligonucleotide probe

<400> 64
atcatcacag attcccgagc 20

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaccttcca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
cgcggcactg atccccacag gtgatgggca gaatctgttt acgaaagacg 50

<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

<400> 68
ggggcggtg gacgcggact cgaacgcagt tgcttcggga cccaggacct 50
cctcgggccc gaccgcccag gaaagactga ggccgcgccc tgccccgccc 100
ggctccctgc gccgcgcgcg cctcccggga cagaagatgt gctccagggt 150
ccctctgctg ctgccgctgc tctgtctact ggccctgggg cctgggggtgc 200
agggctgccc atccggetgc cagtgcagcc agccacagac agtcttctgc 250
actgcccgcc aggggaccac ggtgccccga gacgtgccac ccgacacggt 300
ggggctgtac gtctttgaga acggcatcac catgctcgac gcaagcagct 350
ttgcgggect gccgggectg cagctcctgg acctgtcaca gaaccagatc 400

gccagcctgc	gcctgccccg	cctgctgctg	ctggacctca	gccacaacag	450
cctcctggcc	ctggagcccc	gcctcctgga	cactgccaac	gtggaggcgc	500
tgcggctggc	tggctctggg	ctgcagcagc	tggacgagg	gctcttcagc	550
cgcttgcgca	acctccacga	cctggatgtg	tccgacaacc	agctggagcg	600
agtgccacct	gtgatccgag	gcctccgggg	cctgacgcgc	ctgcggctgg	650
ccggcaacac	ccgcattgcc	cagctgcggc	ccgaggacct	ggccggcctg	700
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 aaaaa 2555

<210> 69
 <211> 598
 <212> PRT
 <213> Homo Sapien

<400> 69
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 Ala Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys
 20 25 30
 Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr
 35 40 45
 Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe
 50 55 60
 Glu Asn Gly Ile Thr Met Leu Asp Ala Ser Ser Phe Ala Gly Leu
 65 70 75
 Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser
 80 85 90
 Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu Ser His Asn Ser
 95 100 105
 Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu

110	115	120
Ala Leu Arg Leu	Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly	
125	130	135
Leu Phe Ser Arg	Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp	
140	145	150
Asn Gln Leu Glu	Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly	
155	160	165
Leu Thr Arg Leu	Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu	
170	175	180
Arg Pro Glu Asp	Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp	
185	190	195
Val Ser Asn Leu	Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly	
200	205	210
Leu Phe Pro Arg	Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe	
215	220	225
Asn Cys Val Cys	Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu	
230	235	240
Ser His Val Thr	Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe	
245	250	255
Pro Pro Lys Asn	Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala	
260	265	270
Asp Phe Gly Cys	Pro Ala Thr Thr Thr Thr Ala Thr Val Pro Thr	
275	280	285
Thr Arg Pro Val	Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu	
290	295	300
Ala Pro Thr Trp	Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro	
305	310	315
Ser Pro Pro Ser	Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln	
320	325	330
Pro Gln Asp Cys	Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys	
335	340	345
His Leu Gly Thr	Arg His His Leu Ala Cys Leu Cys Pro Glu Gly	
350	355	360
Phe Thr Gly Leu	Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg	
365	370	375
Pro Ser Pro Thr	Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr	
380	385	390
Leu Gly Ile Glu	Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu	
395	400	405

Gln Arg Tyr Leu	Gln Gly Ser Ser Val	Gln Leu Arg Ser Leu Arg
410	415	420
Leu Thr Tyr Arg	Asn Leu Ser Gly Pro	Asp Lys Arg Leu Val Thr
425	430	435
Leu Arg Leu Pro	Ala Ser Leu Ala Glu	Tyr Thr Val Thr Gln Leu
440	445	450
Arg Pro Asn Ala	Thr Tyr Ser Val Cys	Val Met Pro Leu Gly Pro
455	460	465
Gly Arg Val Pro	Glu Gly Glu Glu Ala	Cys Gly Glu Ala His Thr
470	475	480
Pro Pro Ala Val	His Ser Asn His Ala	Pro Val Thr Gln Ala Arg
485	490	495
Glu Gly Asn Leu	Pro Leu Leu Ile Ala	Pro Ala Leu Ala Ala Val
500	505	510
Leu Leu Ala Ala	Leu Ala Ala Val Gly	Ala Ala Tyr Cys Val Arg
515	520	525
Arg Gly Arg Ala	Met Ala Ala Ala Ala	Gln Asp Lys Gly Gln Val
530	535	540
Gly Pro Gly Ala	Gly Pro Leu Glu Leu	Glu Gly Val Lys Val Pro
545	550	555
Leu Glu Pro Gly	Pro Lys Ala Thr Glu	Gly Gly Gly Glu Ala Leu
560	565	570
Pro Ser Gly Ser	Glu Cys Glu Val Pro	Leu Met Gly Phe Pro Gly
575	580	585
Pro Gly Leu Gln	Ser Pro Leu His Ala	Lys Pro Tyr Ile
590	595	

<210> 70

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ccctccactg cccacccgac tg 22

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71
cggttctggg gacgtaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
ctgcccaccg tccacctgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
aggactgcc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
ggcactagga caaccttctt cctttctgca ccaactgcccg tacccttacc 50
cgccccgcca cctccttgct accccactct tgaaaccaca gctgttgcca 100
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ggcctccagg caacatgggg ggcccagtca gagagccggc actctcagtt 200
gccctctggt tgagttgggg ggcagctctg ggggccgtgg cttgtgccat 250
ggctctgctg acccaacaaa cagagctgca gagcctcagg agagaggtga 300
gccggctgca ggggacagga ggccctccc agaatgggga agggatatccc 350
tggcagagtc tcccggagca gaggttccgat gccctggaag cctgggagaa 400

tggggagaga tcccggaaaa ggagagcagt gctcacccaa aaacagaaga 450
 agcagcactc tgtcctgcac ctggttccca ttaacgccac ctccaaggat 500
 gactccgatg tgacagaggt gatgtggcaa ccagctctta ggctgtggag 550
 aggcctacag gccaaggat atggtgtccg aatccaggat gctggagttt 600
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 caggtggtgt ctcgagaagg ccaaggaagg caggagactc tattccgatg 700
 tataagaagt atgccctccc acccggaccg ggctacaac agctgctata 750
 ggcaggtgt cttccattta caccaagggg atattctgag tgcataatt 800
 ccccgggcaa gggcgaaact taacctctct ccacatggaa ctttctggg 850
 gtttgtgaaa ctgtgattgt gttataaaaa gtggctccca gcttgaaga 900
 ccaggggtggg tacatactgg agacagccaa gagctgagta tataaaggag 950
 aggaatgtg caggaacaga ggcattcttc tgggtttggc tccccgttc 1000
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 cttgcttctg ttcccatgg agctccg 1077

<210> 76
 <211> 250
 <212> PRT
 <213> Homo Sapien

<400> 76
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro
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 Gly Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala
 20 25 30
 Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala
 35 40 45
 Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg
 50 55 60
 Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
 65 70 75
 Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala
 80 85 90
 Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala
 95 100 105
 Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His Leu
 110 115 120

Val Pro Ile Asn Ala Thr Ser Lys Asp Asp Ser Asp Val Thr Glu
125 130 135

Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln Ala
140 145 150

Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu
155 160 165

Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln
170 175 180

Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg
185 190 195

Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
200 205 210

Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu
215 220 225

Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
230 235 240

His Gly Thr Phe Leu Gly Phe Val Lys Leu
245 250

<210> 77
<211> 2849
<212> DNA
<213> Homo Sapien

<400> 77
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gggggggacc tgtggctgct cgtaccgccc cccaccctcc tcttctgcac 150

tgccgtcttc cggaagacct tttcccctgc tctgttttct tcaccgagtc 200

tgtgcatcgc cccggacctg gccgggagga ggcttggccg gcgggagatg 250

ctctaggggc ggcgcgggag gagcggccgg cgggacggag ggcccggcag 300

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ttgcctttgc ctctggcctg gtcctgagtc gtgtgcccc tgtccagggg 400

gaacagcagg agtgggaggg gactgaggag ctgccgtcgc ctccggacca 450

tgccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500

aggggctccc tgcttcccgg tgcttgcgct gctgtgaccc cggtagctcc 550

atgtaccggc cgaccgccgt gcccagatc aacatcacta tcttgaaagg 600

ggagaagggt gaccgcggag atcgaggcct ccaagggaaa tatggcaaaa 650

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<211> 281

<213> Homo Sapien

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Leu Ala Phe Ala Ser Gly Leu Val Leu Ser Arg Val Pro His Val
20 25 30

Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
35 40 45

Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr
50 55 60

Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
65 70 75

Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro
80 85 90

Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
95 100 105

Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly

110	115	120
Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly		
125	130	135
Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val		
140	145	150
Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val		
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met		
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe		
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His		
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val		
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu		
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg		
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe		
260	265	270
Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro		
275	280	

<210> 79
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 79
 tacaggccca gtcaggacca gggg 24

<210> 80
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 80
 ctgaagaagt agaggccggg cacg 24

<210> 81

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
cccgggtgctt gcgctgctgt gaccccggtg cctccatgta cccgg 45

<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

<400> 82
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ggcgccgggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150
cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200
gacaaaaact aaactgaaat ttaaaatggt cttcggggga gaaggagct 250
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cttcccagcc acagctggcc accacagctc cacctgtaac cactgtcact 1050

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tccaacttaa	ctttgaacac	agggaatgtg	tataacccta	ctgcactttc	1250
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tatgcaaaga	aacagggttag	gacatctagg	ttccaattca	ttcacattct	2150
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<210> 83

<212> PRT

<400> 83

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Ser	Lys	Gly	Ile	Arg	Gly	Asn	Glu	Pro	Val	Tyr	Thr	Ser	Thr	Gln	50	55	60
Glu	Asp	Cys	Ile	Asn	Ser	Cys	Cys	Ser	Thr	Lys	Asn	Ile	Ser	Gly	65	70	75
Asp	Lys	Ala	Cys	Asn	Leu	Met	Ile	Phe	Asp	Thr	Arg	Lys	Thr	Ala	80	85	90
Arg	Gln	Pro	Asn	Cys	Tyr	Leu	Phe	Phe	Cys	Pro	Asn	Glu	Glu	Ala	95	100	105
Cys	Pro	Leu	Lys	Pro	Ala	Lys	Gly	Leu	Met	Ser	Tyr	Arg	Ile	Ile	110	115	120
Thr	Asp	Phe	Pro	Ser	Leu	Thr	Arg	Asn	Leu	Pro	Ser	Gln	Glu	Leu	125	130	135
Pro	Gln	Glu	Asp	Ser	Leu	Leu	His	Gly	Gln	Phe	Ser	Gln	Ala	Val	140	145	150
Thr	Pro	Leu	Ala	His	His	His	Thr	Asp	Tyr	Ser	Lys	Pro	Thr	Asp	155	160	165
Ile	Ser	Trp	Arg	Asp	Thr	Leu	Ser	Gln	Lys	Phe	Gly	Ser	Ser	Asp	170	175	180
His	Leu	Glu	Lys	Leu	Phe	Lys	Met	Asp	Glu	Ala	Ser	Ala	Gln	Leu	185	190	195
Leu	Ala	Tyr	Lys	Glu	Lys	Gly	His	Ser	Gln	Ser	Ser	Gln	Phe	Ser	200	205	210
Ser	Asp	Gln	Glu	Ile	Ala	His	Leu	Leu	Pro	Glu	Asn	Val	Ser	Ala	215	220	225
Leu	Pro	Ala	Thr	Val	Ala	Val	Ala	Ser	Pro	His	Thr	Thr	Ser	Ala	230	235	240
Thr	Pro	Lys	Pro	Ala	Thr	Leu	Leu	Pro	Thr	Asn	Ala	Ser	Val	Thr	245	250	255
Pro	Ser	Gly	Thr	Ser	Gln	Pro	Gln	Leu	Ala	Thr	Thr	Ala	Pro	Pro	260	265	270
Val	Thr	Thr	Val	Thr	Ser	Gln	Pro	Pro	Thr	Thr	Leu	Ile	Ser	Thr	275	280	285
Val	Phe	Thr	Arg	Ala	Ala	Ala	Thr	Leu	Gln	Ala	Met	Ala	Thr	Thr	290	295	300
Ala	Val	Leu	Thr	Thr	Thr	Phe	Gln	Ala	Pro	Thr	Asp	Ser	Lys	Gly			

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Ser Leu Glu Thr	Ile Pro Phe Thr Glu	Ile Ser Asn Leu Thr	Leu		
	320		325		330
Asn Thr Gly Asn	Val Tyr Asn Pro Thr	Ala Leu Ser Met Ser	Asn		
	335		340		345
Val Glu Ser Ser	Thr Met Asn Lys Thr	Ala Ser Trp Glu Gly	Arg		
	350		355		360
Glu Ala Ser Pro	Gly Ser Ser Ser Gln	Gly Ser Val Pro Glu	Asn		
	365		370		375
Gln Tyr Gly Leu	Pro Phe Glu Lys Trp	Leu Leu Ile Gly Ser	Leu		
	380		385		390
Leu Phe Gly Val	Leu Phe Leu Val Ile	Gly Leu Val Leu Leu	Gly		
	395		400		405
Arg Ile Leu Ser	Glu Ser Leu Arg Arg	Lys Arg Tyr Ser Arg	Leu		
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 Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
 50 55 60
 Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
 65 70 75
 Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile
 80 85 90
 Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
 95 100 105
 Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
 110 115 120
 Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser
 125 130 135
 Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
 140 145 150
 Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
 155 160 165

Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser Lys Glu Ile Arg
170 175 180

Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
185 190 195

Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn His Ser
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